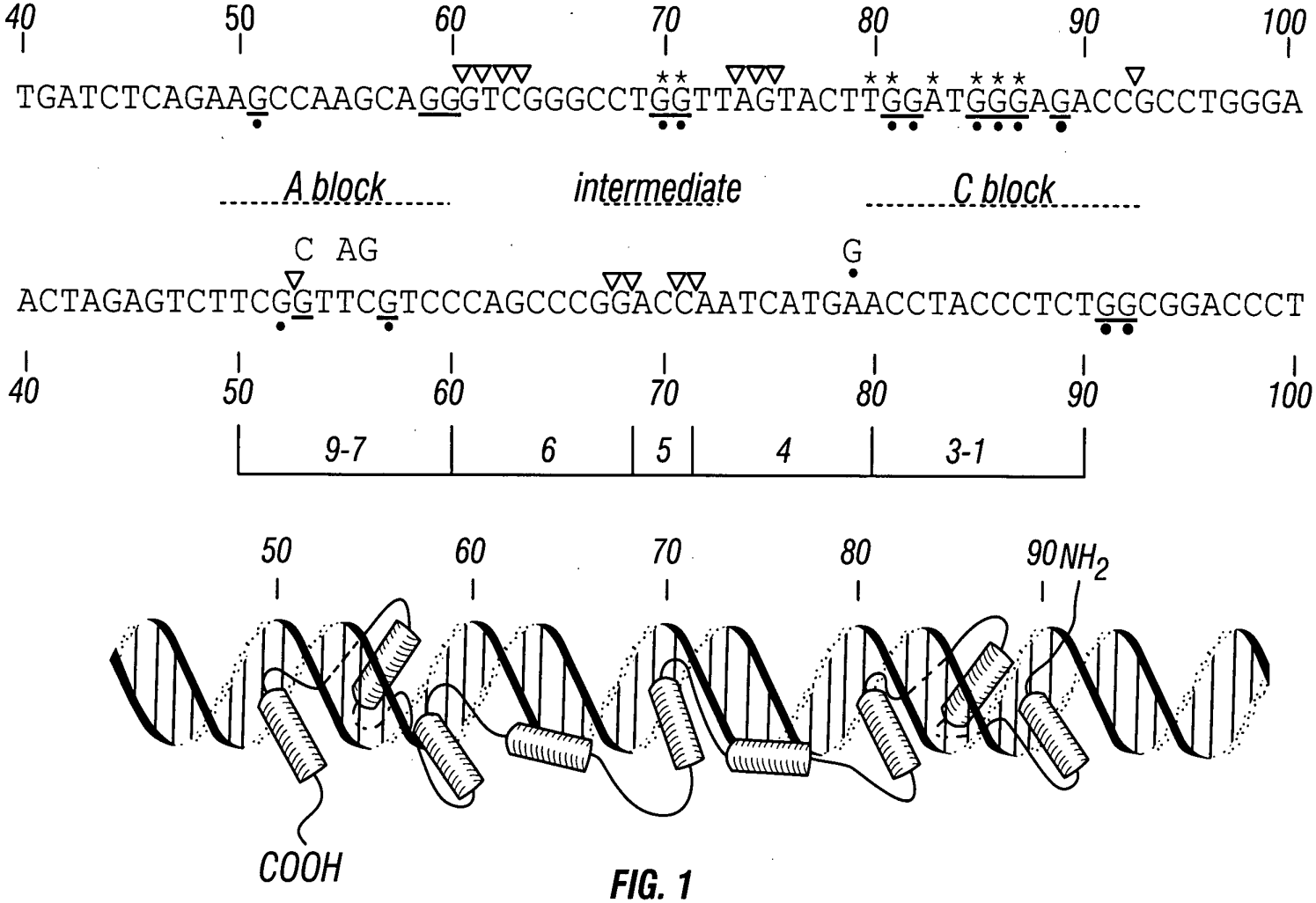
40
50
60
70
80
90
100
TGATCTCAGAAGCCAAGCAGGGTCGGGCCTGGTTAGTACTTGGATGGGAGACCGCCTGGGA
A block
intermediate
C block
C AG
G
ACTAGAGTCTTCGGTTCGTCCCAGCCCGGACCAATCATGAACCTACCCTCTGGCGGACCCT
40
50
60
70
80
90
100
9-7
6
5
4
3-1
50
60
70
80
90
NH2
COOH

FIG. 1

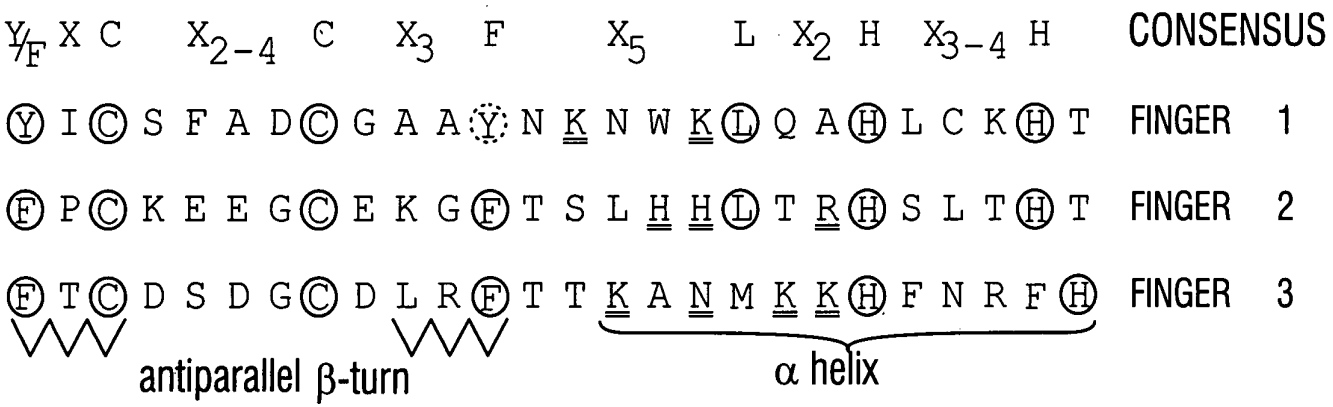
Y/F X C X2-4 C X3 F X5 L X2 H X3-4 H CONSENSUS
Ⓨ I Ⓒ S F A D Ⓒ G A A Ⓨ N K N W K Ⓛ Q A Ⓗ L C K Ⓗ T FINGER 1
Ⓕ P Ⓒ K E E G Ⓒ E K G Ⓕ T S L H H Ⓛ T R Ⓗ S L T Ⓗ T FINGER 2
Ⓕ T Ⓒ D S D G Ⓒ D L R Ⓕ T T K A N M K K Ⓗ F N R F Ⓗ FINGER 3
antiparallel β-turn
α helix

FIG. 2A

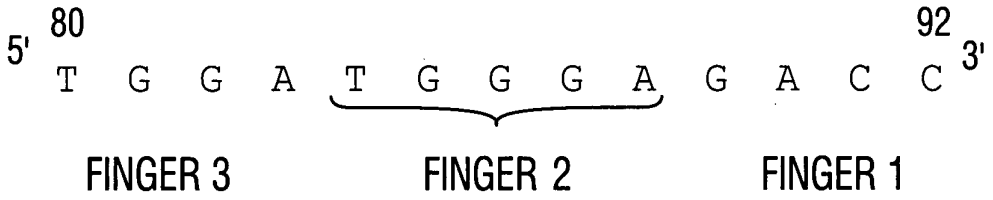
5'
80
T G G A T G G G A G A C C
92
3'
FINGER 3
FINGER 2
FINGER 1

FIG. 2B

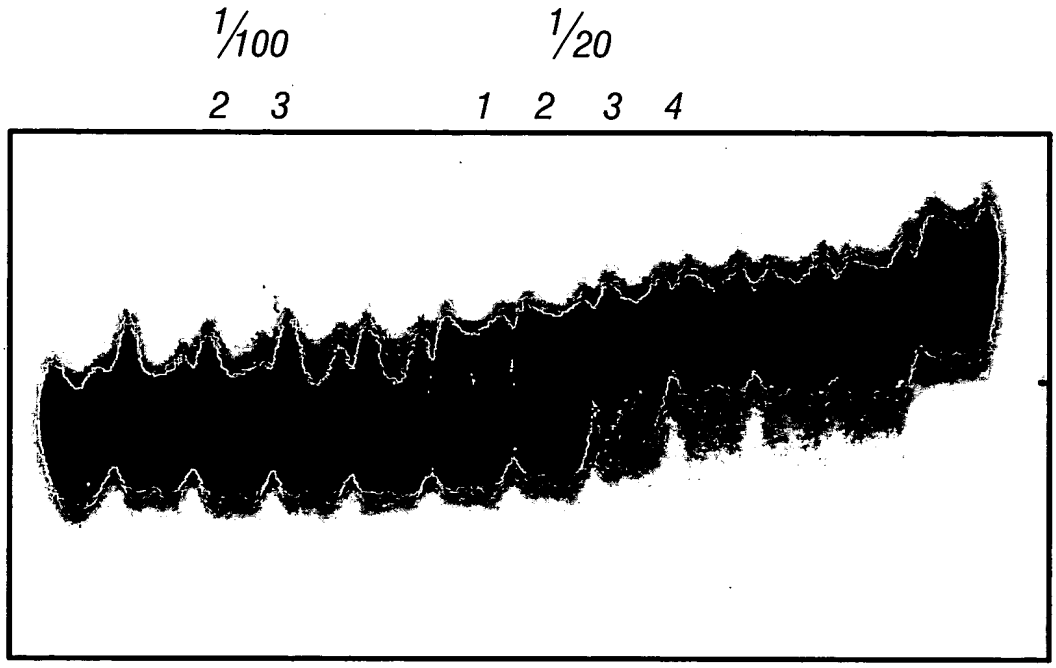

FIG. 3

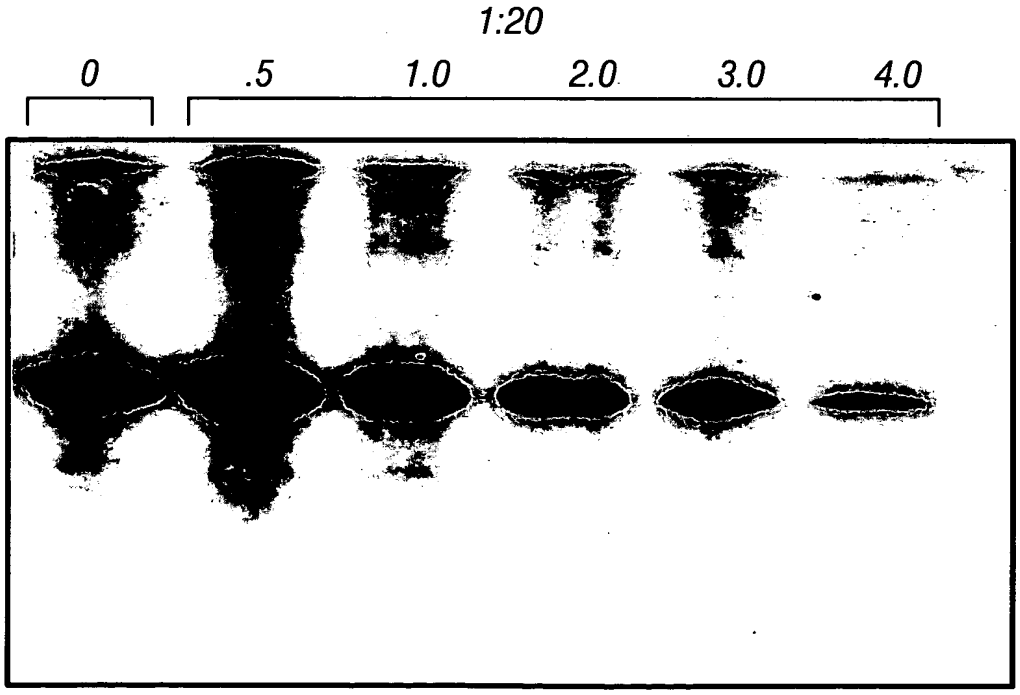

FIG. 4

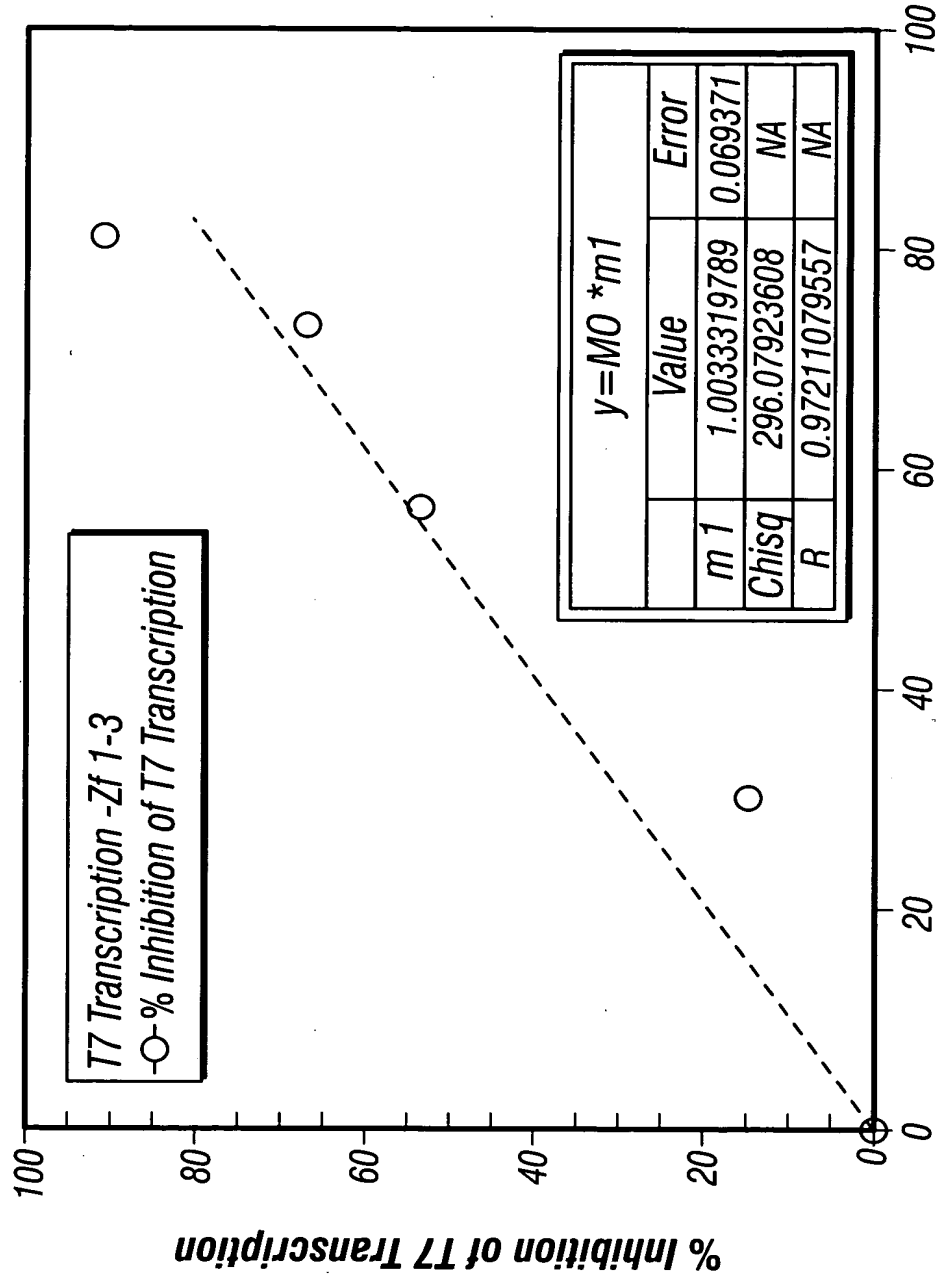
T7 Transcription -Zf 1-3
% Inhibition of T7 Transcription
y=MO *m1
Value
Error
m 1
1.0033319789
0.069371
Chisq
296.07923608
NA
R
0.97211079557
NA
% Inhibition of T7 Transcription
% DNA Molecules Bound by Zf 1-3
0
20
40
60
80
100

FIG. 5

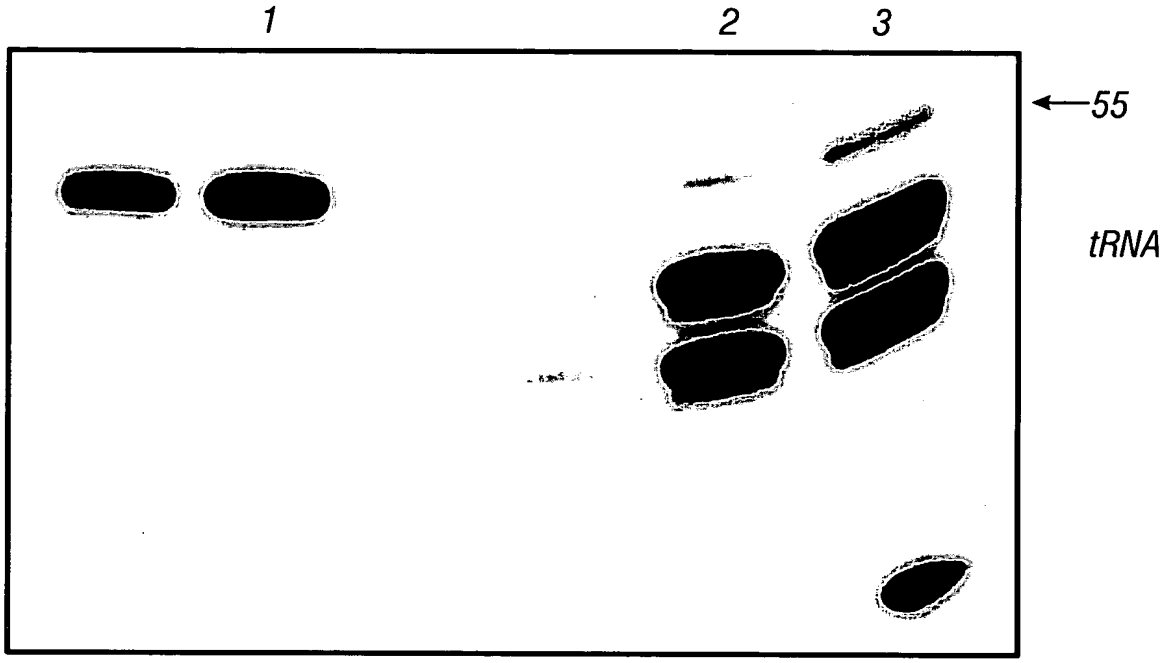

FIG. 6

```
          10                  20                  30                  40
          *                   *                   *                   *
CTC GAG CCC TAT GCT TGC CCT GTC GAG TCC TGC GAT CGC CGC TTT TCT
GAG CTC GGG ATA CGA ACG GGA CAG CTC AGG ACG CTA GCG GCG AAA AGA
 L   E   P   Y   A   C   P   V   E   S   C   D   R   R   E   S>

 50                  60                  70                  80                  90
 *                   *                   *                   *                   *
GGC TCG GAT GAG CTT ACC CGC CAT ATC CGC ATC CAC ACA GGC CAG AAG
GCG AGC CTA CTC GAA TGG GCG GTA TAG GCG TAG GTG TGT CCG GTC TTC
 R   S   D   E   L   T   R   E   I   R   I   E   T   G   Q   R>

100                 110                 120                 130                 140
    *                   *                   *                   *                   *
CCC TTC CAG TGT CGA ATA TGC ATG CGT AAC TTC AGT CGT AGT GAC CAC
GGG AAG GTC ACA GCT TAT ACG TAC GCA TTG AAG TCA GCA TCA CTG GTG
 P   F   Q   C   R   T   C   M   R   N   F   S   R   S   D   R>
```

FIG. 7A

```
          150         160         170         180         190
          *           *           *           *           *
CTT ACC ACC CAC ATC CGC ACC CAC ACA GGC GAG AAG CCT TTT GCC TGT
GAA TGG TGG GTG TAG GCG TGG GTG TGT CCG CTC TTC GGA AAA CGG ACA
 L   T   T   H   I   R   T   E   T   G   E   K   P   F   A   C>

          200         210         220         230         240
          *           *           *           *           *
GAC ATT TGT GGG AGG AAG TTT GCC AGG AGT GAT GAA CGC AAG AGG CAT
CTG TAA ACA CCC TCC TTC AAA CGG TCC TCA CTA CTT GCG TTC TCC GTA
 D   I   C   G   R   K   F   A   R   S   D   E   R   K   R   E>

          250         260         270
          *           *           *
ACG AAA ATC CAT TTA AGA CAG AAG GAC ACT AGT
TGG TTT TAG GTA AAT TCT GTC TTC CTG TGA TCA
 T   K   I   E   L   R   Q   K   E   T   S>
```

FIG. 7B

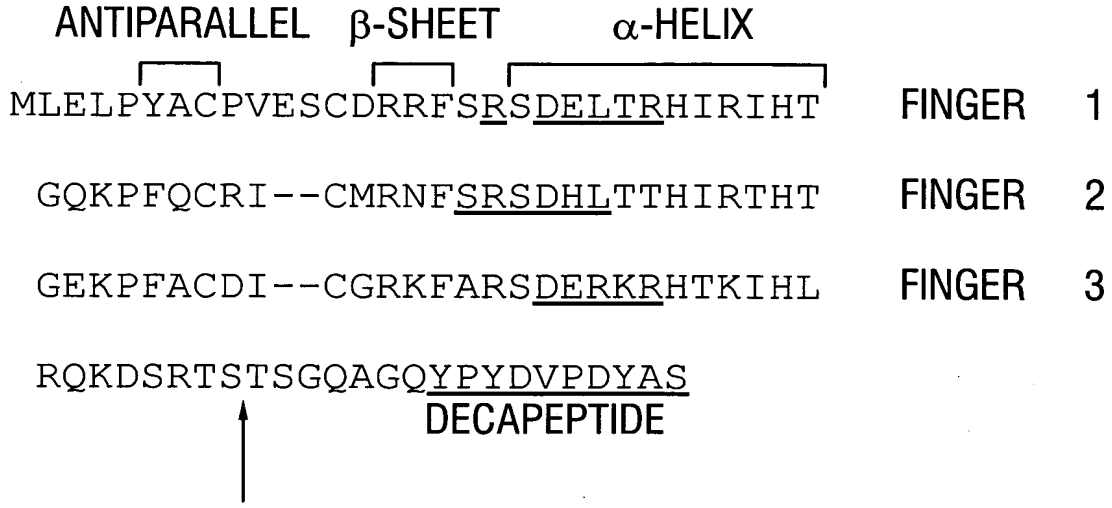
ANTIPARALLEL
β-SHEET
α-HELIX
MLELPYACPVESCDRRFSRSDELTRHIRIHT
FINGER 1
GQKPFQCRI--CMRNFSRSDHLTTHIRTHT
FINGER 2
GEKPFACDI--CGRKFARSDERKRHTKIHL
FINGER 3
RQKDSRTSTSGQAGQYPYDVPDYAS
DECAPEPTIDE

FIG. 8A

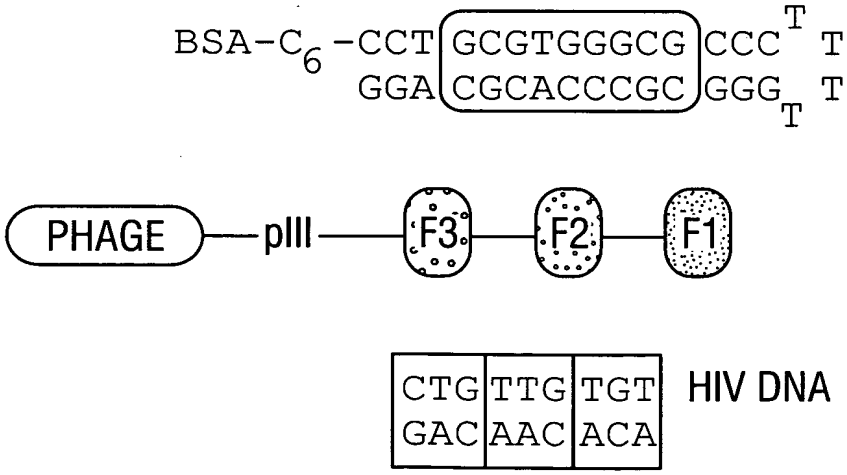
BSA-C6 -CCT GCGTGGGCG CCC T T
GGA CGCACCCGC GGG T T
PHAGE
pIII
F3
F2
F1
CTG TTG TGT
GAC AAC ACA
HIV DNA

FIG. 8B

AMINO ACID SEQUENCES OF SELECTED ZINC FINGER PROTEINS					
FINGER 1	SELECTION		FINGER 2	SELECTION	
GCG	TGT		TGG	TTG	
-123456	-123456		-2-11234	-2-11234	
RDELTR-(WT)			SRSDHL-(WT)		
KADLKR-(C7)	QTASKA-(F8)		TYLNTP	GVTMQP-(G3)	
KCVRGR-(C9)	PTHLQT-(F15)		GYRAAP	PQPLSD	
KCDRGR	PERTQP		LYRYHL	REQVSR-(G4)	
KYCRTR	TSEADH		PTLVNA	THMWMI	
KQLPWT-(C10)	SEQRYP		VRPHQR	QRMRTL-(G5)	
KNSQHP	HQQNKP		PFCPYR	QRVGLF	
KCQMDS	RGQGMA			LRTGNY-(G6)	
QQVTRT	RARQTG			EREFSL	
TQSQSP	ENSFTD			EKESRG	
VHIQAN	NVMGHD			EGVRKN	
	NRGQRK			TGVNSI	
	SRPSQW			TQARPP	
	TSEADH			THMWMI	

FINGER 3	SELECTION
GCG	CTG
-123456	-123456
RDERKR-(WT)	
RDLANS	NVGDKP
SGQWWR-(A14)	SWICGI
SLLVIA	IAWMEL
VSVRGL	IMMTFF
	RECRML
	IALLDT
	NVQGLR

FIG. 9

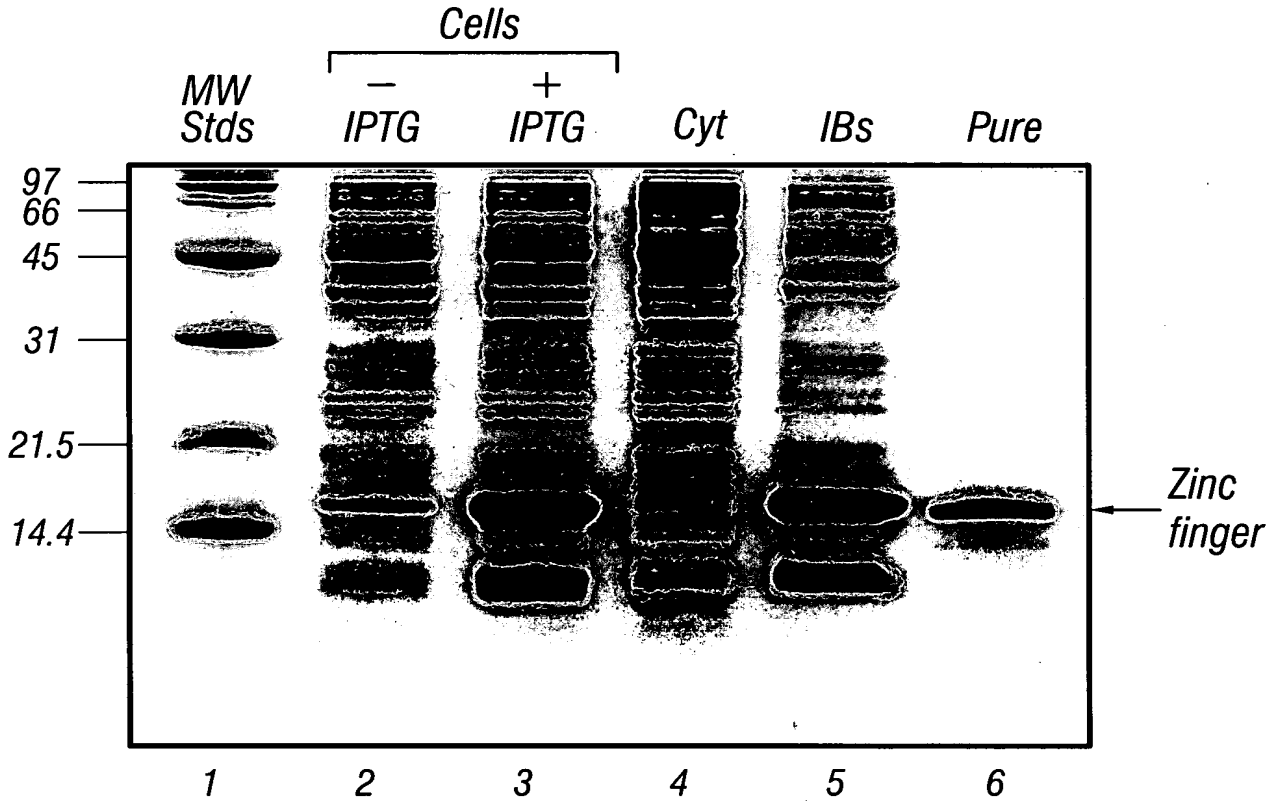
Cells
MW Stds
–
IPTG
+
IPTG
Cyt
IBs
Pure
97
66
45
31
21.5
14.4
Zinc finger
1
2
3
4
5
6

FIG. 10

KINETIC AND EQUALIBRIUM DISSOCIATION CONSTANTS OF ZINC FINGER PROTEINS					
ZINC FINGER PROTEIN	BINDING SITE	$K_{ON}(X10^4)$ $(M^{-1}s^{-1})$	K_{OFF} $(x\ 10^{-4})$ (s^{-1})	$K_d(x10^{-9})$ (M)	K_d/K_d (TARGET)
WT	GCG	3.0±0.04	2.0±0.1	6.5	1
	TGT	1.1±0.2	9.0±1.0	81.8	12.6
	GCG	2.4±0.4	1.5±0.7	6.3	
C7	GCG	8.0±0.7	0.4±0.1	0.5	1
	TGT	0.9±0.1	4.9±2.0	54.4	108.8
C9	GCG	2.0±0.2	1.3±0.3	6.5	1
	TGT	0.9±0.1	23.0 ±3.0	255.6	39.3
C10	GCG	1.8±0.1	4.5±2.0	25.0	1
	TGT	0.3±0.002	1.4±0.1	46.7	1.9
F8	TGT	3.7±1.0	11.0 ±1.5	29.7	1
	GCG	4.8±0.1	52.0 ±0.9	108.3	3.6
F15	TGT	1.9±0.1	7.9±1.0	41.6	1
	GCG	0.9±0.3	17.0 ±1.7	188.9	4.5
G3	TTG	1.7±0.2	2.7±0.2	15.9	1
	TGG	2.7±0.3	6.0±0.2	22.2	1.4
G4	TTG	3.3±0.2	2.1±0.1	6.4	1
	TGG	2.5±0.6	5.7±0.2	22.8	3.6
G5	TTG	0.8±0.1	2.2±0.02	27.5	1
	TGG	1.9±0.2	9.1±0.1	47.9	1.7
G6	TTG	10.0 ±1.0	4.6±0.3	4.6	1
	TGG	0.7±0.1	1.4±0.1	20.0	4.3
A14	GCG	1.3±0.1	1.7±0.0	13.1	1
	CTG	0.2±0.0	10.0 ±0.4	500.0	38.2

FIG. 11

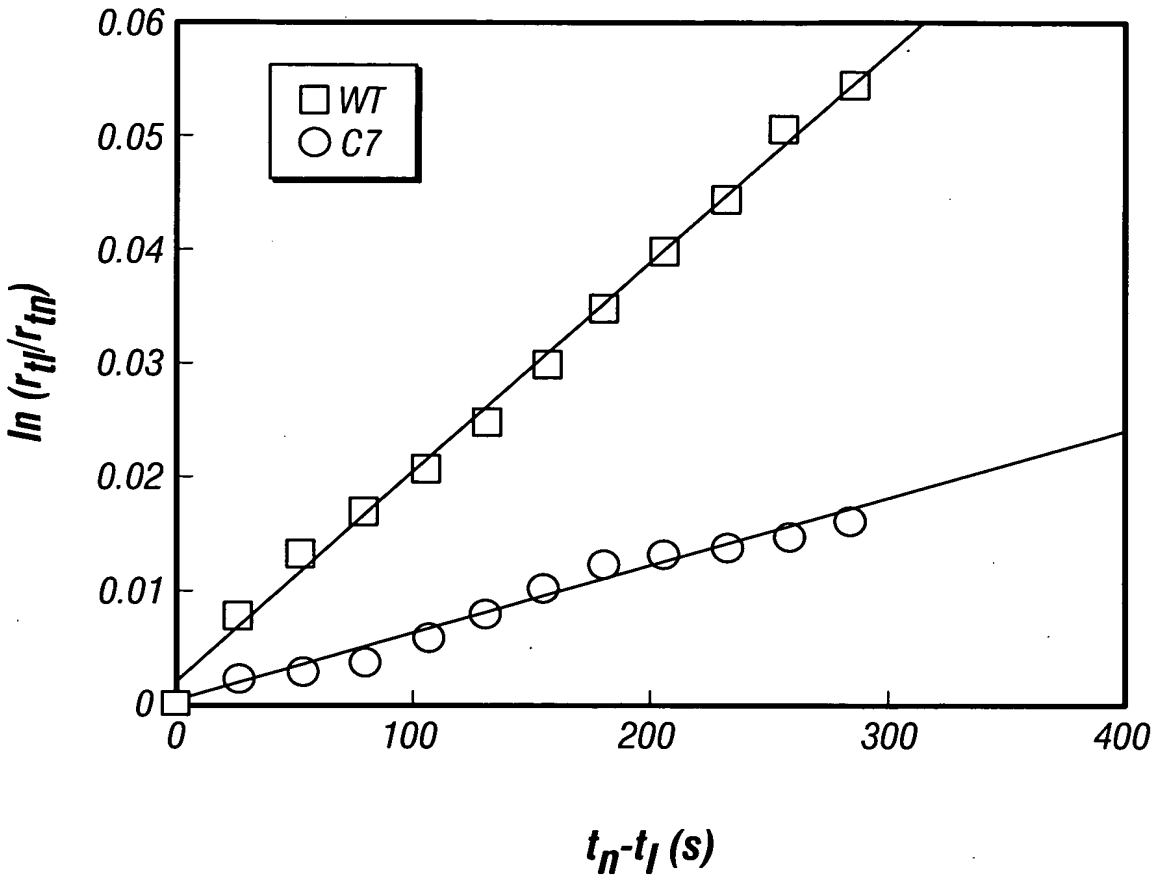

FIG. 12

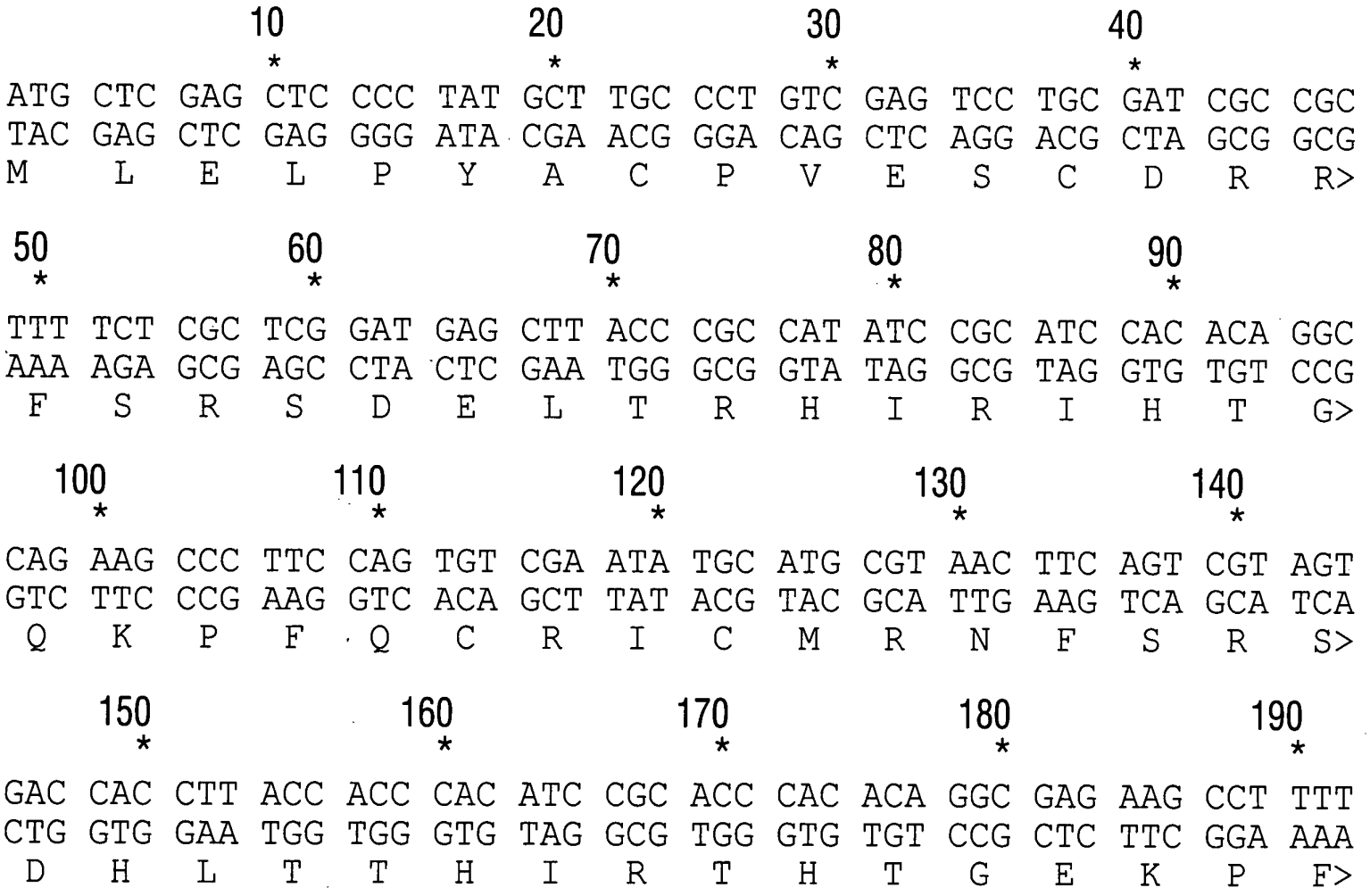
10 20 30 40
ATG CTC GAG CTC CCC TAT GCT TGC CCT GTC GAG TCC TGC GAT CGC CGC
TAC GAG CTC GAG GGG ATA CGA ACG GGA CAG CTC AGG ACG CTA GCG GCG
M L E L P Y A C P V E S C D R R>
50 60 70 80 90
TTT TCT CGC TCG GAT GAG CTT ACC CGC CAT ATC CGC ATC CAC ACA GGC
AAA AGA GCG AGC CTA CTC GAA TGG GCG GTA TAG GCG TAG GTG TGT CCG
F S R S D E L T R H I R I H T G>
100 110 120 130 140
CAG AAG CCC TTC CAG TGT CGA ATA TGC ATG CGT AAC TTC AGT CGT AGT
GTC TTC CGG AAG GTC ACA GCT TAT ACG TAC GCA TTG AAG TCA GCA TCA
Q K P F Q C R I C M R N F S R S>
150 160 170 180 190
GAC CAC CTT ACC ACC CAC ATC CGC ACC CAC ACA GGC GAG AAG CCT TTT
CTG GTG GAA TGG TGG GTG TAG GCG TGG GTG TGT CCG CTC TTC GGA AAA
D H L T T H I R T H T G E K P F>

FIG. 13A-1

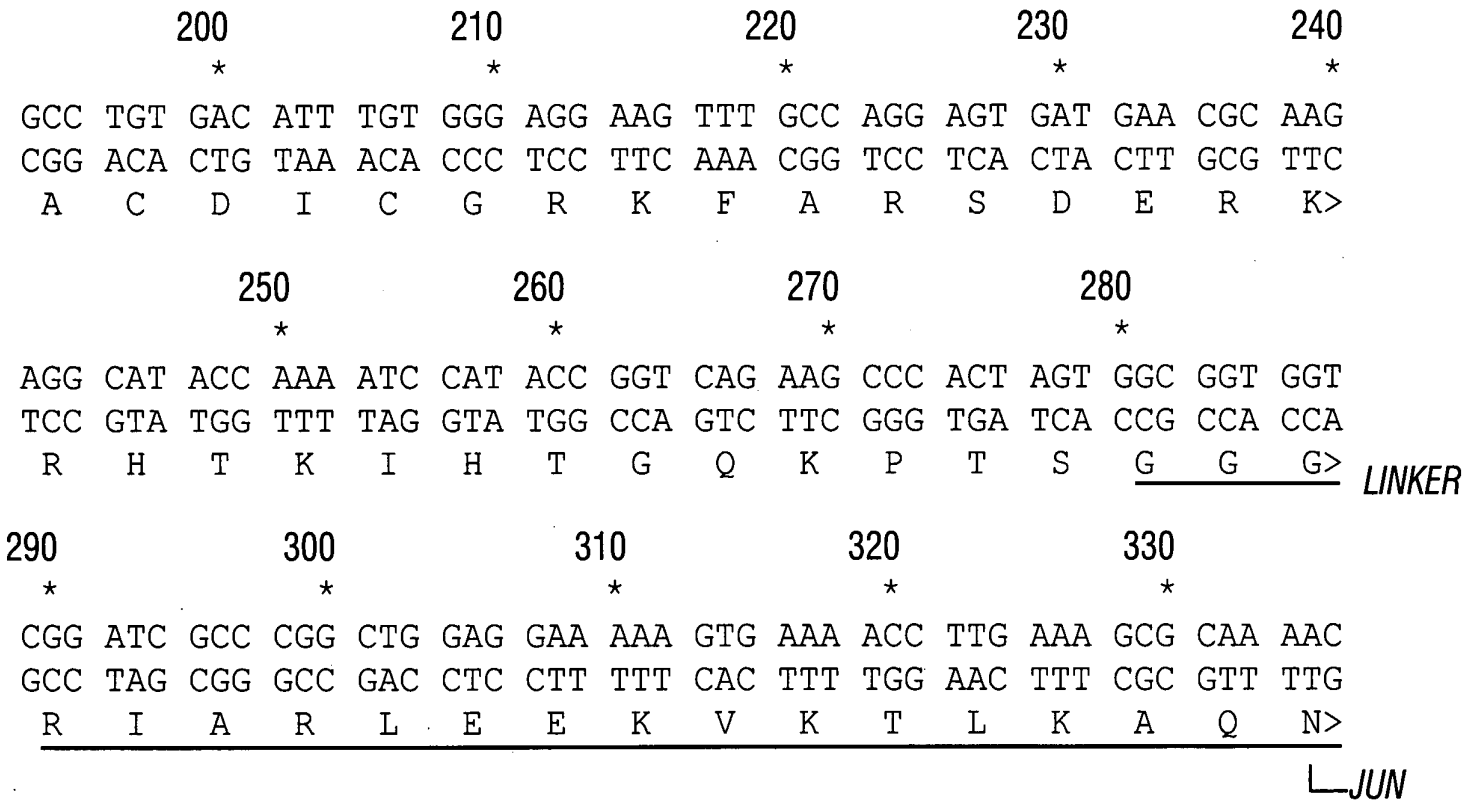
200 210 220 230 240
GCC TGT GAC ATT TGT GGG AGG AAG TTT GCC AGG AGT GAT GAA CGC AAG
CGG ACA CTG TAA ACA CCC TCC TTC AAA CGG TCC TCA CTA CTT GCG TTC
A C D I C G R K F A R S D E R K>
250 260 270 280
AGG CAT ACC AAA ATC CAT ACC GGT CAG AAG CCC ACT AGT GGC GGT GGT
TCC GTA TGG TTT TAG GTA TGG CCA GTC TTC GGG TGA TCA CCG CCA CCA
R H T K I H T G Q K P T S G G G>
LINKER
290 300 310 320 330
CGG ATC GCC CGG CTG GAG GAA AAA GTG AAA ACC TTG AAA GCG CAA AAC
GCC TAG CGG GCC GAC CTC CTT TTT CAC TTT TGG AAC TTT CGC GTT TTG
R I A R L E E K V K T L K A Q N>
JUN

FIG. 13A-2

```
   340         350         360         370         380
    *           *           *           *           *
TCC GAG CTG GCG TCC ACC GCC AAC ATG CTC AGG GAA CAG GTG GCA CAG
AGG CTC GAC CGC AGG TGC CGG TTG TAC GAG TCC CTT GTC CAC CGT GTC
 S   E   L   A   S   T   A   N   M   L   R   E   Q   V   A   Q>

    390         400         410         420         430
     *           *           *           *           *
CTT AAA CAG AAA GTC ATG AAC CAC GCT AGC GGC CAG GCC GGC CAG TAC
GAA TTT GTC TTT CAG TAC TTC GTG CGA TCG CCG GTC CGG CCG GTC ATG
 L   K   Q   K   V   M   N   H   A   S   G   Q   A   G   Q   Y>

        440         450         460
         *           *           *
CCG TAC GAC GTT CCG GAC TAC GCT TCT TAA
GGC ATG CTG CAA GGC CTG ATG CGA AGA ATT
 P   Y   D   V   P   D   Y   A   S   *>
```

DECAPEPTIDE TAG

FIG. 13B

```
          10          20          30          40
           *           *           *           *
ATG CTC GAG CTC CCC TAT GCT TGC CCT GTC GAG TCC TGC GAT CGC CGC
TAC GAG CTC GAG GGG ATA CGA ACG GGA CAG CTC AGG ACG CTA GCG GCG
 M   L   E   L   P   Y   A   C   P   V   E   S   C   D   R   R>

50          60          70          80          90
 *           *           *           *           *
TTT TCT CGC TCG GAT GAG CTT ACC CGC CAT ATC CGC ATC CAC ACA GGC
AAA AGA GCG AGC CTA CTC GAA TGG GCG GTA TAG GCG TAG GTG TGT CCG
 F   S   R   S   D   E   L   T   R   H   I   R   I   H   T   G>

  100         110         120         130         140
   *           *           *           *           *
CAG AAG CCC TTC CAG TGT CGA ATA TGC ATG CGT AAC TTC AGT CGT AGT
GTC TTC GGG AAG GTC ACA GCT TAT ACG TAC GCA TTG AAG TCA GCA TCA
 Q   K   P   F   Q   C   R   I   C   M   R   N   F   S   R   S>

    150         160         170         180         190
     *           *           *           *           *
GAC CAC CTT ACC ACC CAC ATC CGC ACC CAC ACA GGC GAG AAG CCT TTT
CTG GTG GAA TGG TGG GTG TAG GCG TGG GTG TGT CGG CTC TTC GGA AAA
 D   H   L   T   T   H   I   R   T   H   T   G   E   K   P   F>
```

FIG. 14A-1

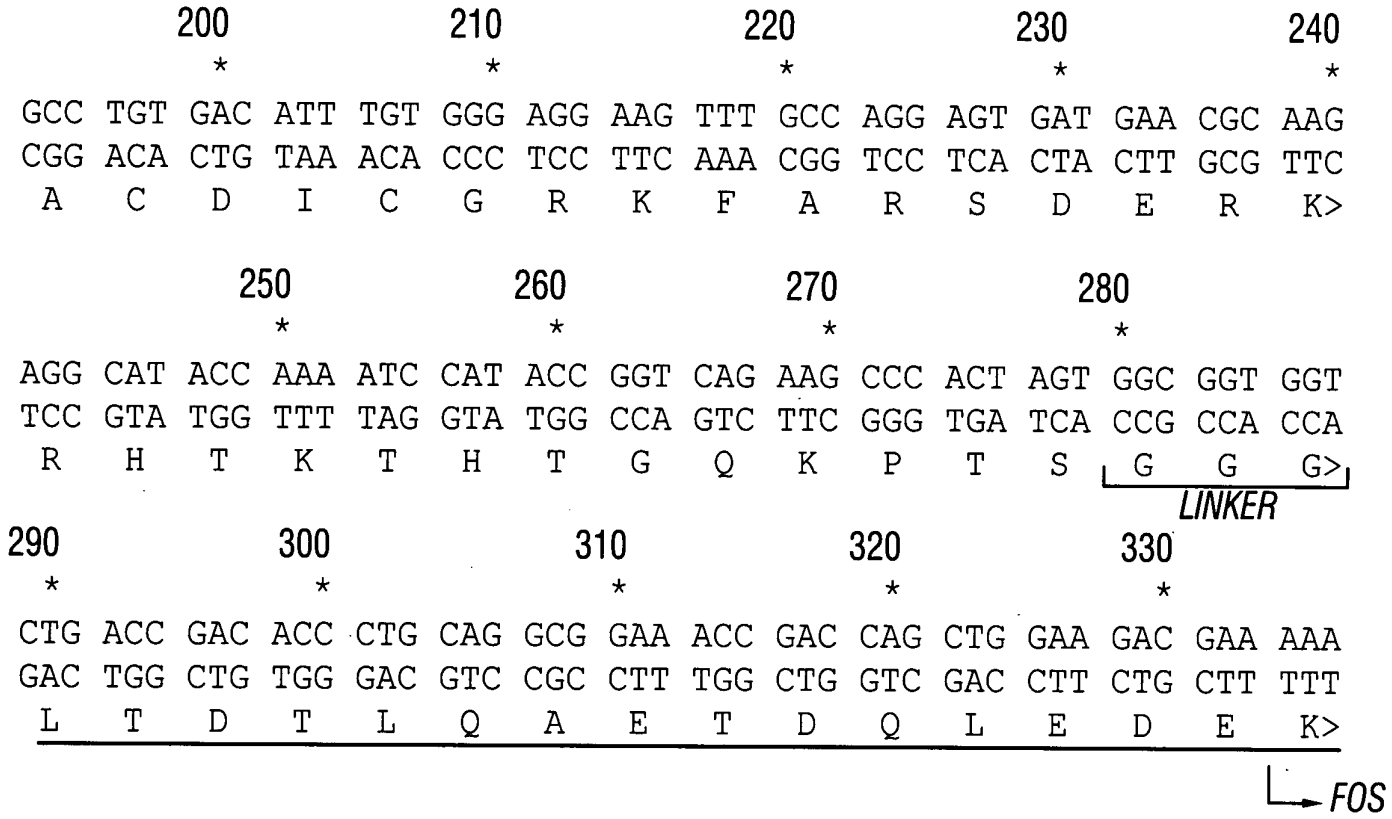
200
210
220
230
240
GCC TGT GAC ATT TGT GGG AGG AAG TTT GCC AGG AGT GAT GAA CGC AAG
CGG ACA CTG TAA ACA CCC TCC TTC AAA CGG TCC TCA CTA CTT GCG TTC
A C D I C G R K F A R S D E R K>
250
260
270
280
AGG CAT ACC AAA ATC CAT ACC GGT CAG AAG CCC ACT AGT GGC GGT GGT
TCC GTA TGG TTT TAG GTA TGG CCA GTC TTC GGG TGA TCA CCG CCA CCA
R H T K T H T G Q K P T S G G G>
LINKER
290
300
310
320
330
CTG ACC GAC ACC CTG CAG GCG GAA ACC GAC CAG CTG GAA GAC GAA AAA
GAC TGG CTG TGG GAC GTC CGC CTT TGG CTG GTC GAC CTT CTG CTT TTT
L T D T L Q A E T D Q L E D E K>
FOS

FIG. 14A-2

```
    340         350         360         370         380
     *           *           *           *           *
TCC GCG CTG CAA ACC GAA ATC GCG AAC CTG CTG AAA GAA AAA GAA AAG
AGG CGC GAC GTT TGG CTT TAG CGC TTG GAC GAC TTT CTT TTT CTT TTC
 S   A   L   Q   T   E   I   A   N   L   L   K   E   K   E   K>

    390         400         410         420         430
     *           *           *           *           *
CTG GAG TTC ATC CTG GCG GCA CAC GCT AGC GGC CAG CCC GGC CAG TAC
GAC TGG CTG TGG GAC GTC CGC CTT TGG CTG GTC GAC CTT CTG CTT TTT
 L   E   F   I   L   A   A   H   A   S   G   Q   A   G   Q   Y>

        440         450         460
         *           *           *
CCG TAC GAC GTT CCG GAC TAC GCT TCT TAA
GGC ATG CTG CAA GGC CTG ATG CGA AGA ATT
 P   Y   D   V   P   D   Y   A   S   *>
```

DECAPEPTIDE TAG

FIG. 14B

```
          10                  20                  30                  40
           *                   *                   *                   *
ATG AAA CTG CTC GAG CCC TAT GCT TGC CCT GTC GAG TCC TGC GAT CGC
TAC TTT GAC GAG CTC GGG ATA CGA ACG GGA CAG CTC AGG ACG CTA GCG
 M   K   L   L   E   P   Y   A   C   P   V   E   S   C   D   R>

 50                  60                  70                  80                  90
  *                   *                   *                   *                   *
CGC TTT TCT AAG TCG GCT GAT CTG AAG CGC CAT ATC CGC ATC CAC ACT
GCG AAA AGA TTC AGC CGA CTA GAC TTC GCG GTA TAG GCG TAG GTG TGA
 R   F   S   K   S   A   D   L   K   R   H   I   R   I   H   T>

   100                 110                 120                 130                 140
    *                   *                   *                   *                   *
GGC GAA AAA CCG TAC GCG TGC CCT GTC GAG TCC TGC GAT CGC CGC TTT
CCG CTT TTT GGC ATG CGC ACG GGA CAG CTC AGG ACG CTA GCG GCG AAA
 G   E   K   P   Y   A   C   P   V   E   S   C   D   R   R   F>

     150                 160                 170                 180                 190
      *                   *                   *                   *                   *
TCT AAG TCG GCT GAT CTG AAG CGC CAT ATC CGC ATC CAC ACC GGG GAG
AGA TTC AGC CGA CTA GAC TTC GCG GTA TAG GCG TAG GTG TGG CCC CTC
 S   K   S   A   D   L   K   R   H   I   R   I   H   T   G   E>
```

FIG. 15A

```
      200         210         220         230         240
       *           *           *           *           *
AAG CCC TAT GCT TGC CCT GTC GAG TCC TGC GAT CGC CGC TTT TCT AAG
TTC GGG ATA CGA ACG GGA CAG CTC AGG ACG CTA GCG GCG AAA AGA TTC
 K   P   Y   A   C   P   V   E   S   C   D   R   R   F   S   K>

          250         260         270         280
           *           *           *           *
TCG GCT GAT CTG AAG CGC CAT ATC CGC ATC CAC ACC GGT CAG AAG CCC
AGC CGA CTA GAC TTC GCG GTA TAG GCG TAG GTG TGG CCA GTC TTC GGG
 S   A   D   L   K   R   H   I   R   I   N   T   G   Q   K   P>

290
 *
ACT ACT
TGA TCA
 T   S>
```

FIG. 15B

```
          10          20          30          40
           *           *           *           *
ATG CTC GAG CTC CCC TAT GCT TGC CCT GTC GAG TCC TGC GAT CGC CGC
TAC GAG CTC GAG GGG ATA CGA ACG GGA CAG CTC AGG ACG CTA GCG GCG
 M   L   E   L   P   Y   A   C   P   V   E   S   C   D   R   R>

50          60          70          80          90
 *           *           *           *           *
TTT TCT CGC TCG GAT GAG CTT ACC CGC CAT ATC CGC ATC CAC ACA GGC
AAA AGA GCG AGC CTA CTC GAA TGG GCG GTA TAG GCG TAG GTG TGT CCG
 F   S   R   S   D   E   L   T   R   H   I   R   I   H   T   G>

100         110         120         130         140
 *           *           *           *           *
CAG AAG CCC TTC CAG TGT CGA ATA TGC ATG CGT AAC TTC AGT CGT AGT
GTC TTC GGG AAG GTC ACA CCT TAT ACG TAC GCA TTG AAG TCA GCA TCA
 Q   K   P   F   Q   C   R   I   C   M   R   N   F   S   R   S>

150         160         170         180         190
 *           *           *           *           *
GAC CAC CTT ACC ACC CAC ATC CGC ACC CAC ACA GGC GAG AAG CCT TTT
CTG GTG GAA TGG TGG GTG TAG GCG TGG GTG TGT CCG CTC TTC GGA AAA
 D   H   L   T   T   H   I   R   T   H   T   G   E   K   P   F>
```

FIG. 16A-1

```
        200           210           220           230           240
         *             *             *             *             *
GCC TGT GAC ATT TGT GGG AGG AAG TTT GCC AGG AGT GAT GAA CGC AAG
CGG ACA CTG TAA ACA CCC TCC TTC AAA CGG TCC TCA CTA CTT GCG TTC
 A   C   D   I   C   G   R   K   F   A   R   S   D   E   R   K>

            250           260           270           280
             *             *             *             *
AGG CAT ACC AAA ATC CAT ACC GGG GAG AAG CCC TAT GCT TGC CCT GTC
TCC GTA TGG TTT TAG GTA TGG CCC CTC TTC GGG ATA CGA ACG GGA CAG
 R   H   T   K   I   H   T   G   E   K   P   Y   A   C   P   V>

290           300           310           320           330
 *             *             *             *             *
GAG TCC TGC GAT CGC CGC TTT TCT CGC TCG GAT GAG CTT ACC CGC CAT
CTC AGG ACG CTA GCG GCG AAA AGA GCG AGC CTA CTC GAA TGG GCG GTA
 E   S   C   D   R   R   F   S   R   S   D   E   L   T   R   H>
```

FIG. 16A-2

```
   340          350          360          370          380
    *            *            *            *            *
ATC CGC ATC CAC ACA GGC CAG AAG CCC TTC CAG TGT CGA ATA TGC ATG
TAG GCG TAG GTG TGT CCG GTC TTC GGG AAG GTC ACA GCT TAT ACG TAC
 I   R   I   H   T   G   Q   K   P   F   Q   C   R   I   C   M>

     390          400          410          420          430
      *            *            *            *            *
CGT AAC TTC AGT CGT AGT GAC CAC CTT ACC ACC CAC ATC CGC ACC CAC
GCA TTG AAG TCA GCA TCA CTG GTG GAA TGG TGG GTG TAC CCC TCC CTG
 R   N   F   S   R   S   D   H   L   T   T   H   I   R   T   H>

        440          450          460          470          480
         *            *            *            *            *
ACA GGC GAG AAG CCT TTT GCC TGT GAC ATT TGT GGG AGG AAG TTT GCC
TGT CCG CTC TTC GGA AAA CGG ACA CTG TAA ACA CCC TCC TTC AAA CGG
 T   G   E   K   P   F   A   C   D   I   C   G   R   K   F   A>

            490          500          510          520
             *            *            *            *
AGG AGT GAT GAA CGC AAG AGG CAT ACC AAA ATC CAT TTA AGA CAG AAG
TCC TCA CTA CTT GCG TTC TCC GTA TGG TTT TAG GTA AAT TCT GTC TTC
 R   S   D   E   R   K   R   H   T   K   I   H   L   R   Q   K>

530          540
 *            *
GAC TCT AGA ACT AGT
CTG AGA TCT TGA TCA
 D   S   R   T   S>
```

FIG. 16B

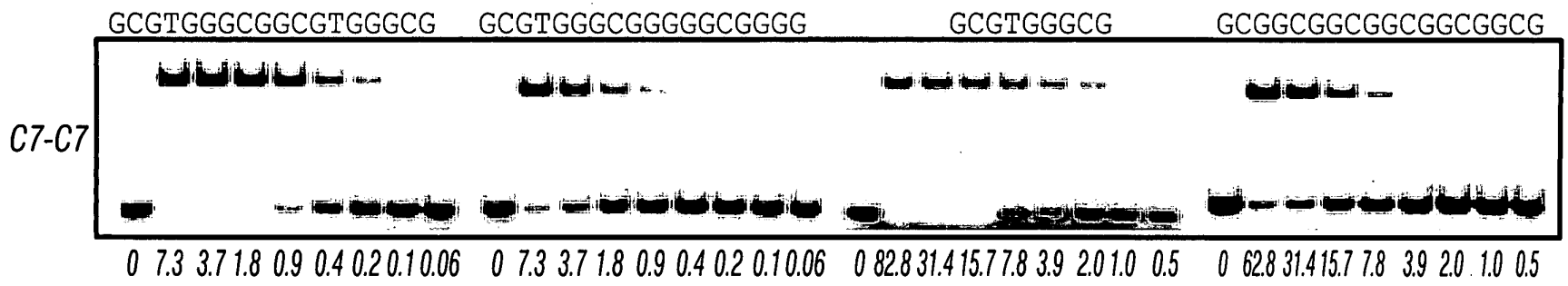

FIG. 17A

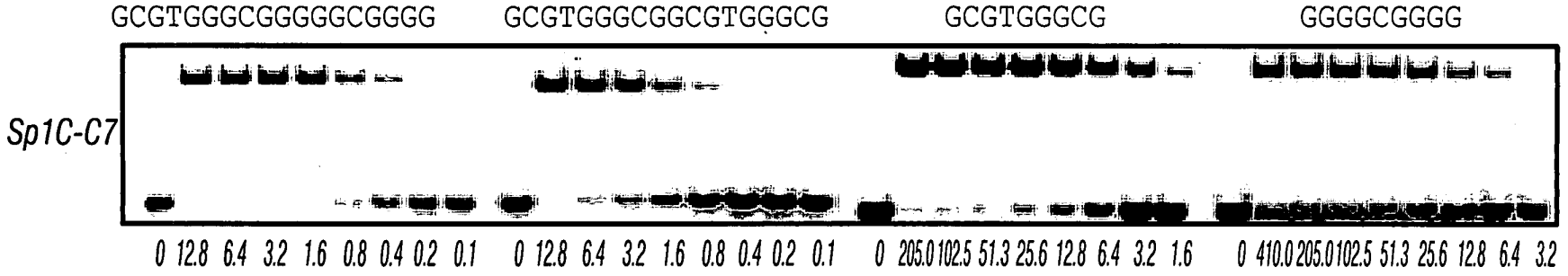

FIG. 17B

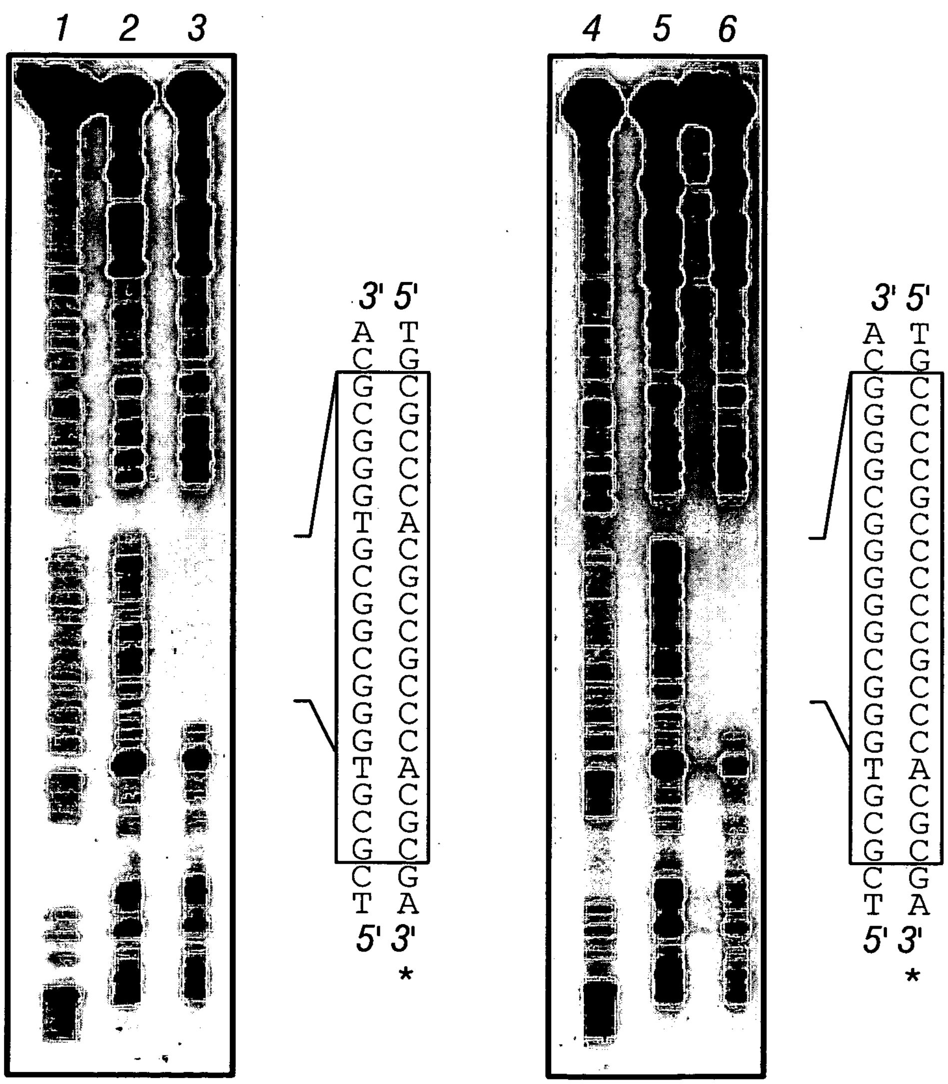
1 2 3
4 5 6
3' 5'
A T
C G
G C
C G
G C
G C
G C
T A
G C
C G
G C
G C
C G
G C
G C
G C
T A
G C
C G
G C
C G
T A
5' 3'
*
3' 5'
A T
C G
G C
G C
G C
G C
C G
G C
G C
G C
G C
G C
C G
G C
G C
G C
T A
G C
C G
G C
C G
T A
5' 3'
*

FIG. 18

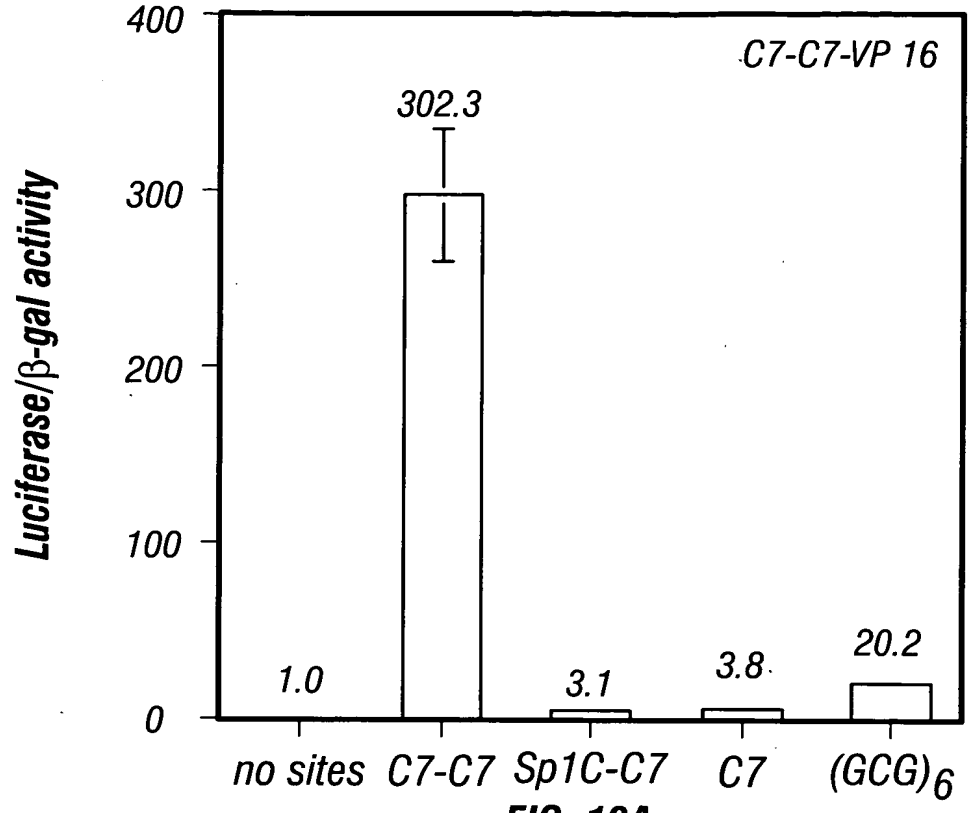

FIG. 19A

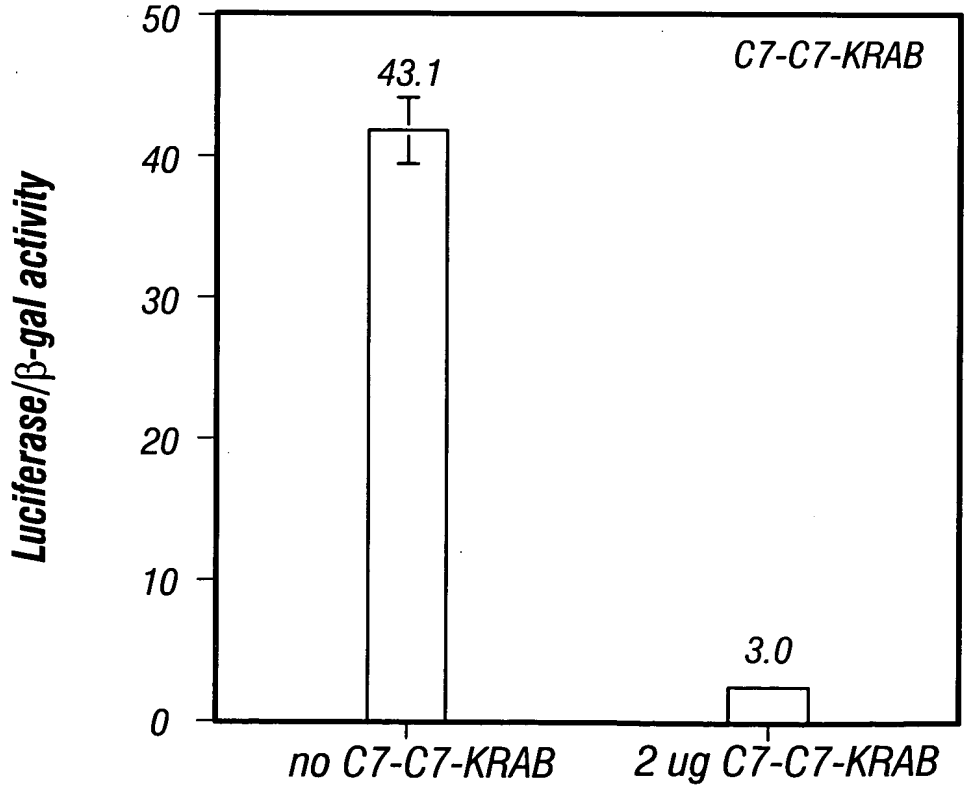

FIG. 19B